NUSeq Core Facility – September 2023 Update

Next-Generation Sequencing, Genomics, and Bioinformatics Research Support

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Introduction

NUSeq is committed to providing state-of-the-art next-generation sequencing (NGS) and other genomics technologies, with integrated bioinformatics support, to Northwestern biomedical research. While the Core operates under the auspices of Center for Genetic Medicine (CGM) and mostly supported by Feinberg, NUSeq supports all NU researchers on both campuses, as well as external organizations. NUSeq has a broad user base with users coming from all bio-related NU departments and research centers, and over 50 external organizations in the U.S. and other countries.

Major genomics technologies available at NUSeq include short reads sequencing, long reads sequencing, single cell and spatial transcriptomics, microarray, Nanostring nCounter, digital and real-time PCR, cell line authentication, DNA/RNA extraction and analysis. Bioinformatics services are provided to projects with genomics data generated in the Core or externally.

Major Core Services

Spatial Transcriptomics
Visualize gene activity in spatial context

Single Cell Sequencing
Gene expression and regulation in thousands up to one million individual cells

Whole Genome Sequencing
Variant identification or de novo assembly of large or small genomes

Whole Exome Sequencing
Exome sequencing for human and other species

RNA Sequencing
Transcriptome analysis at tissue or cell population level

DNA Methylation Sequencing
Epigenomic analysis through bisulfite conversion-based sequencing

ChIP-Seq
For detection of DNA-protein interaction. ChIP-derived DNA needed

ATAC-Seq
For assaying chromatin accessibility

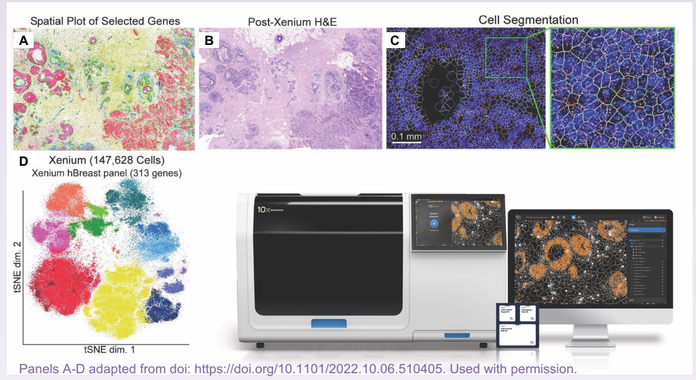
Microbiome Sequencing (16S+ITS and Shotgun Metagenomics)
Microbial community analysis using targeted or shotgun sequencing

Other Genomics Services
NanoString Gene Panel Profiling, DNA Fragmentation/Size Selection, Cell Line Authentication, Digital droplet PCR, Real-Time Quantitative PCR, Illumina Microarray Processing, DNA/RNA Extraction

What's New in Fiscal Year 2024

New Spatial Biology Platform: 10x Xenium In Situ

Spatial gene expression analysis at subcellular resolution



Panels A-D adapted from doi: https://doi.org/10.1101/2022.10.06.510405. Used with permission.

Figure 1. Xenium data from human breast cancer FFPE tissue using a 313-plex gene panel. A - Expression of selected gene markers (*POSTN, IL7R, ITGAX,* etc.); B - H&E staining post Xenium workflow; C - Cell segmentation assigns transcripts to cells; D - t-SNE plot of different cell types in the Xenium data.

State-of-the-Art Illumina Sequencing Technology: NovaSeq X Plus

Continuous evolution of Illumina sequencing technologies to bring down sequencing costs

- Highest throughput from new flow cell design (above)
- Faster speed and better accuracy with new chemistry and optics
- 1.6 – 26 billion reads per flow cell
- Up to 16 Tb per run, >128 human genomes at 30x coverage
- Further improved cost efficiency

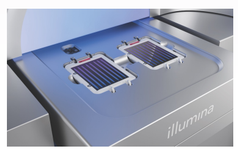


Figure 2. Illumina NovaSeq X Plus (left) and its flow cells (bottom right).

New sequencing options to provide more flexibility and cost effectiveness

The popular Single-End 50 and Paired-End 150 base sequencing can now be ordered at increments of 100 million reads

Major FY2023 Achievements

Establishment of CytAssist Service for Spatial Transcriptomics with 10x Visium

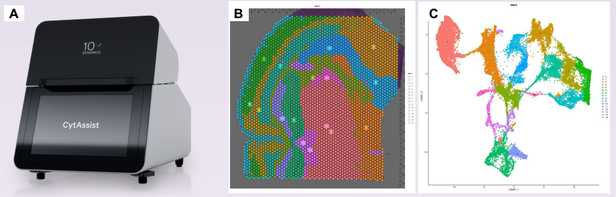


Figure 3. 10x CytAssist (A) enables use of FFPE and pre-existing tissue sections for Visium-based spatial transcriptomics. Panels B-C show Visium data in the brain by region, and clustering of the regions based on their gene expression profiles (PI: M. Martina).

Acquisition of Complete Genomics DNBSEQ-G400

- Two flow cell types: FCS and FCL
- FCS: two lanes, at 300 million reads per lane
- FCL: four lanes, at 400 million reads per lane
- Read length options: SE50, SE100, SE400, PE150, PE200, and PE300
- Improved cost efficiency

Figure 4. The Complete Genomics DNBSEQ-G400 is a mid-level sequencer that offers sample flexibility and quick turnaround time.

Establishment of Oxford Nanopore PromethION for Large-Scale Genome/Transcriptome Long Reads Sequencing

NUSeq FY 2023 Quick Summary

Number of Users: 762
Number of PIs/Groups: 357
- 288 Northwestern PIs/Groups
- 69 External PIs/Groups

Total User Expenditure on NUSeq Services: $3,660,577.98
- 82% of Services Completed for Northwestern Users
- 18% of Services Completed for External Users

Acknowledgment

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